GNCAGCATTTCCTCTAAGGGATNCAATNNGGCTTGCCCGAGGCCACACTCATTTCCCCATNCCC
TCAAATACTGTGGTGATTAAACATTTCATAGGAGGANTTTATGGATNCCTTTAAAANCCTAATT
CTCCCTGCTTGCCAAATCATTTCTTCTCAGCATCCTGCCCAGCAAAAAANCANCTTNTGATCAA
AATNATCCCCGGAGGCTTNACGGAGGCCAGACCTGCCACAGCAGNAGTCCNGGAGATTGCTGAC
CGGGTCAAAGCACAGCTCGANGAGGAAACCAATGAGAAATATGAAATATTCAAAGCCGTTGAGT
ATAAAACTCAAGTTGTCGCTGGAGTCAATTACTTCATTAAGATGGATGTAGGGGGTGGTTGTTT
CACCCACATAAAAGTCTTCAAGGATCTTTCTGGAAAGAATAATTTGGAACTTACTGGTTACCAG
ACTAACAAAACCGAGGATGATGAGCTGACCTACTTCTAAGCAGCAAATTCTAAAGTGACCTGAT
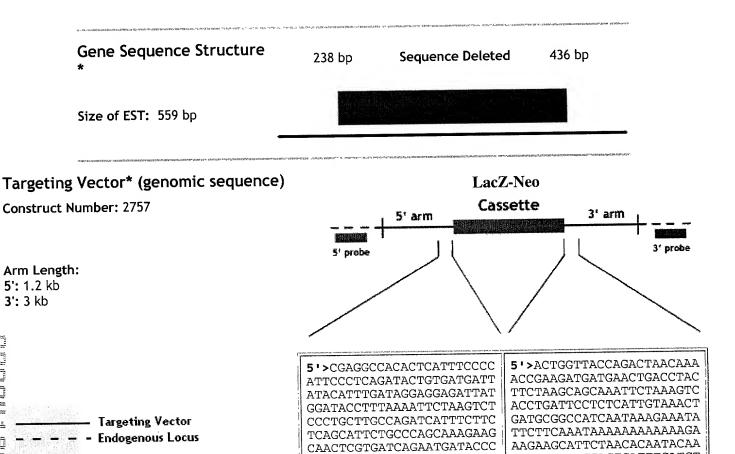TCCTCTCATTGTAAACTGATTCGNCCATCAATAAAGAATATTCTCCA (SEQ ID NO:1)

FIGURE 1

underlined = deleted in targeting construct

[ ] = sequence flanking Neo insert in targeting construct

[GNCAGCATTTCCTCTAAGGGATNCAATNNGGCTTGCCCGAGGCCACACTCATTTCCCCA
TNCCCTCAAATACTGTGGTGATTAAACATTTCATAGGAGGANTTTATGGATNCCTTTAAA
ANCCTAATTCTCCCTGCTTGCCAAATCATTTCTTCTCAGCATCCTGCCCAGCAAAAAANC
ANCTTNTGATCAAAATNATCCCCGGAGGCTTNACGGAGGCCAGACCTGCCACAGCAGN]<u>A
GTCCNGGAGATTGCTGACCGGGTCAAAGCACAGCTCGANGAGGAAACCAATGAGAAATAT
GAAATATTCAAAGCCGTTGAGTATAAAACTCAAGTTGTCGCTGGAGTCAATTACTTCATT
AAGATGGATGTAGGGGGTGGTTGTTTCACCCACATAAAAGTCTTCAAGGATCTTTCTGGA
AAGAATAATTTGGAACTT</u>[ACTGGTTACCAGACTAACAAAACCGAGGATGATGAGCTGAC
CTACTTCTAAGCAGCAAATTCTAAAGTGACCTGATTCCTCTCATTGTAAACTGATTCGNC
CATCAATAAAGAATATTCTCCA]

FIGURE 2A

Gene Sequence Structure *

238 bp   **Sequence Deleted**   436 bp

Size of EST: 559 bp

Targeting Vector* (genomic sequence)

Construct Number: 2757

LacZ-Neo Cassette

Arm Length:
5': 1.2 kb
3': 3 kb

———— Targeting Vector
— — — — Endogenous Locus

* Not drawn to scale

5' arm   3' arm

5' probe   3' probe

```
5'>CGAGGCCACACTCATTTCCCC
ATTCCCTCAGATACTGTGATGATT
ATACATTTGATAGGAGGAGATTAT
GGATACCTTTAAAATTCTAAGTCT
CCCTGCTTGCCAGATCATTTCTTC
TCAGCATTCTGCCCAGCAAAGAAG
CAACTCGTGATCAGAATGATACCC
GGAGGCTTGATGGAGGCCAGACCT
GCCACAGCAGA<3'
(SEQ ID NO:2)
```

```
5'>ACTGGTTACCAGACTAACAAA
ACCGAAGATGATGAACTGACCTAC
TTCTAAGCAGCAAATTCTAAAGTC
ACCTGATTCCTCTCATTGTAAACT
GATGCGGCCATCAATAAAGAAATA
TTCTTCAAATAAAAAAAAAAAAGA
AAGAAGCATTCTAACACAATACAA
TCCAAAGATGTACTGATTTGATGT
TACATACTCAG<3'
(SEQ ID NO:3)
```

FIGURE 2B